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#20 1600
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RAW SEQUENCE LISTING

DATE: 12/05/2002

PATENT APPLICATION: US/09/607,156

TIME: 10:23:40

Input Set : N:\Cr3\RULE60\09607156.raw

Output Set: N:\CRF4\12052002\I607156.raw

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DEC 10 2002

TECH CENTER 1600/2900

SEQUENCE LISTING

ENTERED

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Loetscher, Marcel

6 Moser, Bernhard

8 (ii) TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,

9 NUCLEIC ACIDS, AND METHODS OF USES THEREFOR

11 (iii) NUMBER OF SEQUENCES: 4

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

15 (B) STREET: Two Militia Drive

16 (C) CITY: Lexington

17 (D) STATE: MA

18 (E) COUNTRY: USA

19 (F) ZIP: 02173

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/607,156

C--> 29 (B) FILING DATE: 29-Jun-2000

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: US/08/709,838

34 (B) FILING DATE:

36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: Brook Esq., David E.

38 (B) REGISTRATION NUMBER: 22,592

39 (C) REFERENCE/DOCKET NUMBER: TKI96-01

41 (ix) TELECOMMUNICATION INFORMATION:

42 (A) TELEPHONE: (617) 861-6240

43 (B) TELEFAX: (617) 861-9540

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 1670 base pairs

50 (B) TYPE: nucleic acid

51 (C) STRANDEDNESS: double

52 (D) TOPOLOGY: unknown

56 (ix) FEATURE:

57 (A) NAME/KEY: CDS

58 (B) LOCATION: 69..1172

61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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Input Set : N:\Crif3\RULE60\09607156.raw

Output Set: N:\CRF4\12052002\I607156.raw

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63 CCAACCACAA GCACCAAAGC AGAGGGGCAG GCAGCACACC ACCCAGCAGC CAGAGCACCA      60
65 GCCCAGCC ATG GTC CTT GAG GTG AGT GAC CAC CAA GTG CTA AAT GAC GCC      110
66      Met Val Leu Glu Val Ser Asp His Gln Val Leu Asn Asp Ala
67      1          5          10
70 GAG GTT GCC GCC CTC CTG GAG AAC TTC AGC TCT TCC TAT GAC TAT GGA      158
71 Glu Val Ala Ala Leu Leu Glu Asn Phe Ser Ser Ser Tyr Asp Tyr Gly
72 15          20          25          30
74 GAA AAC GAG AGT GAC TCG TGC TGT ACC TCC CCG CCC TGC CCA CAG GAC      206
75 Glu Asn Glu Ser Asp Ser Cys Cys Thr Ser Pro Pro Cys Pro Gln Asp
76      35          40          45
78 TTC AGC CTG AAC TTC GAC CGG GCC TTC CTG CCA GCC CTC TAC AGC CTC      254
79 Phe Ser Leu Asn Phe Asp Arg Ala Phe Leu Pro Ala Leu Tyr Ser Leu
80      50          55          60
82 CTC TTT CTG CTG GGG CTG CTG GGC AAC GGC GCG GTG GCA GCC GTG CTG      302
83 Leu Phe Leu Leu Gly Leu Leu Gly Asn Gly Ala Val Ala Ala Val Leu
84      65          70          75
86 CTG AGC CGG CGG ACA GCC CTG AGC AGC ACC GAC ACC TTC CTG CTC CAC      350
87 Leu Ser Arg Arg Thr Ala Leu Ser Ser Thr Asp Thr Phe Leu Leu His
88      80          85          90
90 CTA GCT GTA GCA GAC ACG CTG CTG GTG CTG ACA CTG CCG CTC TGG GCA      398
91 Leu Ala Val Ala Asp Thr Leu Leu Val Leu Thr Leu Pro Leu Trp Ala
92 95          100          105          110
94 GTG GAC GCT GCC GTC CAG TGG GTC TTT GGC TCT GGC CTC TGC AAA GTG      446
95 Val Asp Ala Ala Val Gln Trp Val Phe Gly Ser Gly Leu Cys Lys Val
96      115          120          125
98 GCA GGT GCC CTC TTC AAC ATC AAC TTC TAC GCA GGA GCC CTC CTG CTG      494
99 Ala Gly Ala Leu Phe Asn Ile Asn Phe Tyr Ala Gly Ala Leu Leu Leu
100      130          135          140
102 GCC TGC ATC AGC TTT GAC CGC TAC CTG AAC ATA GTT CAT GCC ACC CAG      542
103 Ala Cys Ile Ser Phe Asp Arg Tyr Leu Asn Ile Val His Ala Thr Gln
104      145          150          155
106 CTC TAC CGC CGG GGG CCC CCG GCC CGC GTG ACC CTC ACC TGC CTG GCT      590
107 Leu Tyr Arg Arg Gly Pro Pro Ala Arg Val Thr Leu Thr Cys Leu Ala
108      160          165          170
110 GTC TGG GGG CTC TGC CTG CTT TTC GCC CTC CCA GAC TTC ATC TTC CTG      638
111 Val Trp Gly Leu Cys Leu Leu Phe Ala Leu Pro Asp Phe Ile Phe Leu
112 175          180          185          190
114 TCG GCC CAC CAC GAC GAG CGC CTC AAC GCC ACC CAC TGC CAA TAC AAC      686
115 Ser Ala His His Asp Glu Arg Leu Asn Ala Thr His Cys Gln Tyr Asn
116      195          200          205
118 TTC CCA CAG GTG GGC CGC ACG GCT CTG CGG GTG CTG CAG CTG GTG GCT      734
119 Phe Pro Gln Val Gly Arg Thr Ala Leu Arg Val Leu Gln Leu Val Ala
120      210          215          220
122 GGC TTT CTG CTG CCC CTG CTG GTC ATG GCC TAC TGC TAT GCC CAC ATC      782
123 Gly Phe Leu Leu Pro Leu Leu Val Met Ala Tyr Cys Tyr Ala His Ile
124      225          230          235
126 CTG GCC GTG CTG CTG GTT TCC AGG GGC CAG CGG CGC CTG CGG GCC ATG      830
127 Leu Ala Val Leu Leu Val Ser Arg Gly Gln Arg Arg Leu Arg Ala Met
128      240          245          250

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130 CGG CTG GTG GTG GTG GTC GTG GTG GCC TTT GCC CTC TGC TGG ACC CCC      878
131 Arg Leu Val Val Val Val Val Val Ala Phe Ala Leu Cys Trp Thr Pro
132 255                               260                               265                               270
134 TAT CAC CTG GTG GTG CTG GTG GAC ATC CTC ATG GAC CTG GGC GCT TTG      926
135 Tyr His Leu Val Val Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu
136                               275                               280                               285
138 GCC CGC AAC TGT GGC CGA GAA AGC AGG GTA GAC GTG GCC AAG TCG GTC      974
139 Ala Arg Asn Cys Gly Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val
140                               290                               295                               300
142 ACC TCA GGC CTG GGC TAC ATG CAC TGC TGC CTC AAC CCG CTG CTC TAT      1022
143 Thr Ser Gly Leu Gly Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr
144                               305                               310                               315
146 GCC TTT GTA GGG GTC AAG TTC CGG GAG CGG ATG TGG ATG CTG CTC TTG      1070
147 Ala Phe Val Gly Val Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu
148                               320                               325                               330
150 CGC CTG GGC TGC CCC AAC CAG AGA GGG CTC CAG AGG CAG CCA TCG TCT      1118
151 Arg Leu Gly Cys Pro Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser
152 335                               340                               345                               350
154 TCC CGC CGG GAT TCA TCC TGG TCT GAG ACC TCA GAG GCC TCC TAC TCG      1166
155 Ser Arg Arg Asp Ser Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser
156                               355                               360                               365
158 GGC TTG TGAGCCGGA ATCCGGGCTC CCCTTTCGCC CACAGTCTGA CTTCCTCCGCA      1222
159 Gly Leu
162 TTCCAGGCTC CTCCCTCCCT CTGCCGGCTC TGGCTCTCCC CAATATCCTC GCTCCCGGGA      1282
164 CTCACTGGCA GCCCCAGCAC CACCAGGTCT CCCGGGAAGC CACCTTCCCA GCTCTGAGGA      1342
166 CTGCACCATT GCTGCTCCTT AGCTGCCAAG CCCCATCCTG CCGCCCGAGG TGGCTGCCTG      1402
168 GAGCCCCACT GCCCTTCTCA TTTGGAAAC' AAAAC'TTCAT CTTCCCCAAG TGCGGGGAGT      1462
170 ACAAGGCATG GCGTAGAGGG TGCTGCCCCA TGAAGCCACA GCCCAGGCCT CCAGCTCAGC      1522
172 AGTGACTGTG GCCATGGTCC CCAAGACCTC TATATTTGCT CTTTATTTT TATGTCTAAA      1582
174 ATCCTGCTTA AAAC'TTTCA ATAAACAAGA TCGTCAGGAC CTTTTTTTTT TTTTTTTTTT      1642
176 TTTTTTTTTT TTTTTTTTTT TTTTTTTT      1670
179 (2) INFORMATION FOR SEQ ID NO: 2:
181     (i) SEQUENCE CHARACTERISTICS:
182         (A) LENGTH: 368 amino acids
183         (B) TYPE: amino acid
184         (D) TOPOLOGY: linear
186     (ii) MOLECULE TYPE: protein
188     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
190 Met Val Leu Glu Val Ser Asp His Gln Val Leu Asn Asp Ala Glu Val
191 1 5 10 15
193 Ala Ala Leu Leu Glu Asn Phe Ser Ser Ser Tyr Asp Tyr Gly Glu Asn
194 20 25 30
196 Glu Ser Asp Ser Cys Cys Thr Ser Pro Pro Cys Pro Gln Asp Phe Ser
197 35 40 45
199 Leu Asn Phe Asp Arg Ala Phe Leu Pro Ala Leu Tyr Ser Leu Leu Phe
200 50 55 60
202 Leu Leu Gly Leu Leu Gly Asn Gly Ala Val Ala Ala Val Leu Leu Ser
203 65 70 75 80
205 Arg Arg Thr Ala Leu Ser Ser Thr Asp Thr Phe Leu Leu His Leu Ala

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206          85          90          95
208 Val Ala Asp Thr Leu Leu Val Leu Thr Leu Pro Leu Trp Ala Val Asp
209          100          105          110
211 Ala Ala Val Gln Trp Val Phe Gly Ser Gly Leu Cys Lys Val Ala Gly
212          115          120          125
214 Ala Leu Phe Asn Ile Asn Phe Tyr Ala Gly Ala Leu Leu Ala Cys
215          130          135          140
217 Ile Ser Phe Asp Arg Tyr Leu Asn Ile Val His Ala Thr Gln Leu Tyr
218 145          150          155          160
220 Arg Arg Gly Pro Pro Ala Arg Val Thr Leu Thr Cys Leu Ala Val Trp
221          165          170          175
223 Gly Leu Cys Leu Leu Phe Ala Leu Pro Asp Phe Ile Phe Leu Ser Ala
224          180          185          190
226 His His Asp Glu Arg Leu Asn Ala Thr His Cys Gln Tyr Asn Phe Pro
227          195          200          205
229 Gln Val Gly Arg Thr Ala Leu Arg Val Leu Gln Leu Val Ala Gly Phe
230          210          215          220
232 Leu Leu Pro Leu Leu Val Met Ala Tyr Cys Tyr Ala His Ile Leu Ala
233 225          230          235          240
235 Val Leu Leu Val Ser Arg Gly Gln Arg Arg Leu Arg Ala Met Arg Leu
236          245          250          255
238 Val Val Val Val Val Ala Phe Ala Leu Cys Trp Thr Pro Tyr His
239          260          265          270
241 Leu Val Val Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu Ala Arg
242          275          280          285
244 Asn Cys Gly Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val Thr Ser
245          290          295          300
247 Gly Leu Gly Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr Ala Phe
248 305          310          315          320
250 Val Gly Val Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu Arg Leu
251          325          330          335
253 Gly Cys Pro Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser Ser Arg
254          340          345          350
256 Arg Asp Ser Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser Gly Leu
257          355          360          365

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260 (2) INFORMATION FOR SEQ ID NO: 3:

262 (i) SEQUENCE CHARACTERISTICS:

263 (A) LENGTH: 28 base pairs

264 (B) TYPE: nucleic acid

265 (C) STRANDEDNESS: single

266 (D) TOPOLOGY: unknown

270 (ix) FEATURE:

271 (A) NAME/KEY: modified_base

272 (B) LOCATION: 11

273 (D) OTHER INFORMATION: /mod_base= i

275 (ix) FEATURE:

276 (A) NAME/KEY: modified_base

277 (B) LOCATION: 12

278 (D) OTHER INFORMATION: /mod_base= i

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Input Set : N:\Crf3\RULE60\09607156.raw

Output Set: N:\CRF4\12052002\I607156.raw

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280      (ix) FEATURE:
281          (A) NAME/KEY: modified_base
282          (B) LOCATION: 23
283          (D) OTHER INFORMATION: /mod_base= i
285      (ix) FEATURE:
286          (A) NAME/KEY: modified_base
287          (B) LOCATION: 26
288          (D) OTHER INFORMATION: /mod_base= i
291      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
293 GGGCTGCAGC NNTKKCMGAC MTNCTNYT                28
295 (2) INFORMATION FOR SEQ ID NO: 4:
297      (i) SEQUENCE CHARACTERISTICS:
298          (A) LENGTH: 27 base pairs
299          (B) TYPE: nucleic acid
300          (C) STRANDEDNESS: single
301          (D) TOPOLOGY: unknown
305      (ix) FEATURE:
306          (A) NAME/KEY: modified_base
307          (B) LOCATION: 10
308          (D) OTHER INFORMATION: /mod_base= i
310      (ix) FEATURE:
311          (A) NAME/KEY: modified_base
312          (B) LOCATION: 16
313          (D) OTHER INFORMATION: /mod_base= i
315      (ix) FEATURE:
316          (A) NAME/KEY: modified_base
317          (B) LOCATION: 18
318          (D) OTHER INFORMATION: /mod_base= i
321      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
323 GGGTCTAGAN GGGTTNANRC ARCWRYG                27

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VERIFICATION SUMMARY

DATE: 12/05/2002

PATENT APPLICATION: US/09/607,156

TIME: 10:23:41

Input Set : N:\Crf3\RULE60\09607156.raw

Output Set: N:\CRF4\12052002\I607156.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]